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Volume 993 of the series [Methods in Molecular Biology](#) pp 39-65

Date: 05 March 2013

In Silico Models for Drug Resistance

- Segun Fatumo
- , Marion Adebisi
- , Ezekiel Adebisi

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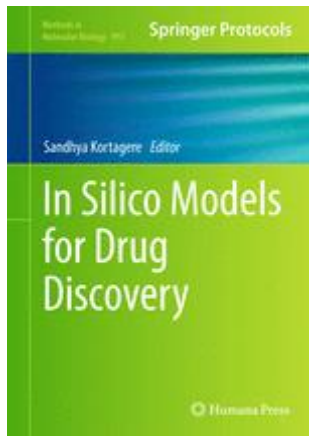
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Abstract

Resistance to drugs that treat infectious disease is a major problem worldwide. The rapid emergence of drug resistance is not well understood. We present two in silico models for the discovery of drug resistance mechanisms and for combating the evolution of resistance, respectively. In the first model, we computationally investigated subgraphs of a biological interaction network that show substantial adaptations when cells transcriptionally respond to a changing environment or treatment. As a case study, we investigated the response of the malaria parasite *Plasmodium falciparum* to chloroquine and tetracycline treatments. The second model involves a machine learning technique that combines clustering, common distance similarity measurements, and hierarchical clustering to propose new combinations of drug targets.

Key words

In silico Drug Resistance Model Mechanism



Chapter 4

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Key words: In silico, Drug, Resistance, Model, Mechanism

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In this paper, we present our in silico models, one for the discovery of drug resistance mechanisms and another for controlling the evolution of drug resistance. Although we have shared and developed these models for malaria research, they can be employed to the study of other infectious diseases. The first model has not been previously published. A model similar to our second model has been developed for the treatment of gastrointestinal cancer (487711). This review summarizes our efforts up to the different types of secondary mutations can occur in the same domain. The aim is to provide an overview of the progress before selecting the right compound that does not produce and group mutations according to the model, enabling clinicians to prescribe an appropriate drug to a patient. Despite a particular situation.

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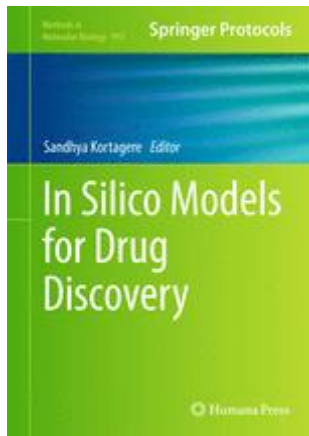
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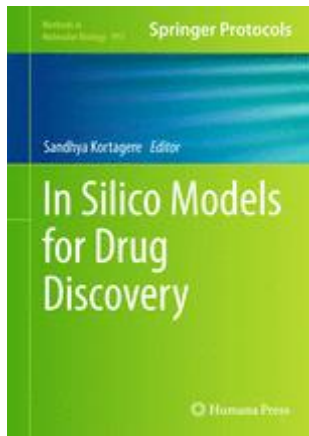
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